

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Shyjan, Andrew W.
- (ii) TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
DIAGNOSIS, PREVENTION AND TREATMENT OF TUMOR
PROGRESSION
- (iii) NUMBER OF SEQUENCES: 9
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Fish & Richardson P.C.
(B) STREET: 225 Franklin Street
(C) CITY: Boston
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02110-2804
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US
(B) FILING DATE: 29-MAR-1996
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/412,431
(B) FILING DATE: 29-MAR-1995
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Fasse, J. Peter
(B) REGISTRATION NUMBER: 32,983
(C) REFERENCE/DOCKET NUMBER: 07334/004001
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 617/542-5070
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(C) TELEX: 200154

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 186 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGTGCTGGAG TACCTCATGG GCGGTGCCTA CCGCTGCAAC TACACTCGGA AAAGCTTCCG 60
GACTCTCTAC AACAACTTGT TTGGCCCTAA GAGGGTAGAG CTCAGCAGAC ACACAGTGTC 120

CTGTGCCTCC CAGAGTAACA TGTGGTTCCT TGATGTGCTT CCCCAAAAGC CCACCTGTGC 180
AGAATG 186

(2) INFORMATION FOR SEQ ID NO:2:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2729 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AAGGAGGCTA GGCTGCACCC TTCCCGCTTG CTCAGCAGCT GAGGCAGGGT CAGAAAGCAT 60
GGATAGAGAA GACATTTTGC AAAAGGGAAT GCATCTTTGT AATTCACAGT ACAAAGACC 120
CTAACAGATG TTGCTGTGGT CAGCTCACTA ACCAGCACAT CCCCCCTTTG CCGAGTGGGG 180
CTCCCAGCAC AACAGGAGAG GACACCAAGC AGGCAGACAC GCAGTCCGGG AAATGGTCTG 240
TCAGCAAACA CACCCAGAGC TACCCAACAG ACTCCTATGG GATTCTTGAA TTCCAGGGTG 300
GGGGTTACTC CAATAAAGCC ATG TAC ATC CGA GTC TCC TAC GAC ACC AAG 350
Met Tyr Ile Arg Val Ser Tyr Asp Thr Lys
1 5 10
CCA GAT TCC CTG CTC CAC CTC ATG GTG AAG GAC TGG CAG CTG GAG CTC 398
Pro Asp Ser Leu Leu His Leu Met Val Lys Asp Trp Gln Leu Glu Leu
15 20 25
CCG AAG CTC TTG ATA TCT GTG CAC GGA GGC CTC CAA AGC TTC GAG ATG 446
Pro Lys Leu Leu Ile Ser Val His Gly Lys Leu Gln Ser Phe Glu Met
30 35 40
CAG TCC AAA CTG AAG CAG GTG TTT GGG AAA GGT CTG ATC AAG GCT GCC 494
Gln Ser Lys Leu Lys Gln Val Phe Gly Lys Gly Leu Ile Lys Ala Ala
45 50 55
ATG ACC ACG GGG GCG TGG ATC TTC ACC GGG GGT GTG AGC ACT GGT GTC 542
Met Thr Thr Gly Ala Trp Ile Phe Thr Gly Gly Val Ser Thr Gly Val
60 65 70
GTC AGC CAT GTG GGG GAT GCC TTG AAA GAC CAC TCC TCC AAG TCC AGA 590
Val Ser His Val Gly Asp Ala Leu Lys Asp His Ser Ser Lys Ser Arg
75 80 85 90
GGC CGG CTC TGT GCT ATA GGA ATT GCT CCC TGG GGC ATG GTG GAG AAC 638
Gly Arg Leu Cys Ala Ile Gly Ile Ala Pro Trp Gly Met Val Glu Asn
95 100 105
AAG GAA GAC CTG ATT GGA AAA GAT GTA ACA AGA GTC TAT CAG ACC ATG 686
Lys Glu Asp Leu Ile Gly Lys Asp Val Thr Arg Val Tyr Gln Thr Met
110 115 120
TCC AAC CCT CTG AGC AAG CTC TCT GTG CTC AAC AAT TCC CAC ACT CAC 734
Ser Asn Pr Leu Ser Lys Leu Ser Val Leu Asn Asn Ser His Thr His

4

125						130						135						
TTC Phe 140	ATC Ile	TTG Leu	GCT Ala	GAC Asp	AAC Asn	GGC Gly 145	ACC Thr	CTG Leu	GGC Gly	AAG Lys	TAT Tyr 150	GGT Gly	GCT Ala	GAG Glu	GTG Val	782		
AAG Lys 155	CTT Leu	CGA Arg	AGA Arg	CAG Gln	CTG Leu 160	GAA Glu	AAA Lys	CAC His	ATC Ile	TCC Ser 165	CTG Leu	CAG Gln	AAG Lys	ATC Ile	AAC Asn 170	830		
ACA Thr	AGG Arg	CTG Leu	GGC Gly	CAG Gln 175	GGT Gly	GTA Val	CCT Pro	GTC Val	GTG Val 180	GGC Gly	CTA Leu	GTG Val	GTA Val	GAA Glu 185	GGT Gly	878		
GGT Gly	CCT Pro	AAC Asn	GTG Val 190	GTT Val	TCT Ser	ATC Ile	GTC Val	CTG Leu 195	GAG Glu	TAT Tyr	CTC Leu	AAA Lys	GAA Glu 200	GAC Asp	CCT Pro	926		
CCT Pro	GTC Val	CCT Pro 205	GTG Val	GTG Val	GTT Val	TGC Cys	GAT Asp 210	GGC Gly	AGT Ser	GGA Gly	CGT Arg	GCC Ala 215	TCT Ser	GAC Asp	ATT Ile	974		
TTG Leu	TCC Ser 220	TTC Phe	GCA Ala	CAC His	AAA Lys	TAC Tyr 225	TGC Cys	GAC Asp	GAA Glu	GGA Gly	GGA Gly 230	GTC Val	ATA Ile	AAC Asn	GAG Glu	1022		
TCC Ser 235	CTG Leu	CGG Arg	GAC Asp	CAG Gln	CTT Leu 240	CTA Leu	GTT Val	ACC Thr	ATT Ile	CAG Gln 245	AAA Lys	ACA Thr	TTT Phe	AAT Asn	TAC Tyr 250	1070		
AGC Ser	AAG Lys	TCC Ser	CAG Gln	TCG Ser 255	TAT Tyr	CAG Gln	CTG Leu	TTT Phe	GCA Ala 260	ATT Ile	ATC Ile	ATG Met	GAG Glu	TGC Cys 265	ATG Met	1118		
AAG Lys	AAG Lys	AAA Lys	GAA Glu 270	CTC Leu	GTC Val	ACT Thr	GTG Val	TTT Phe 275	CGG Arg	ATG Met	GGT Gly	TCC Ser	GAG Glu 280	GGT Gly	CAG Gln	1166		
CAA Gln	GAT Asp	GTC Val 285	GAG Glu	ATG Met	GCA Ala	ATT Ile	TTA Leu 290	ACT Thr	GCC Ala	TTG Leu	CTC Leu	AAA Lys 295	GGA Gly	ACC Thr	AAC Asn	1214		
GCA Ala	TCA Ser 300	GCT Ala	CCA Pro	GAT Asp	CAG Gln	CTG Leu 305	AGC Ser	TTG Leu	GCC Ala	CTG Leu	GCT Ala 310	TGG Trp	AAC Asn	CGG Arg	GTC Val	1262		
GAC Asp 315	ATA Ile	GCG Ala	CGA Arg	AGC Ser	CAG Gln 320	ATC Ile	TTC Phe	GTC Val	TTT Phe	GGC Gly 325	CCA Pro	CAC His	TGG Trp	CCG Pro	CCA Pro 330	1310		
CTG Leu	GGA Gly	AGC Ser	CTG Leu	GCC Ala 335	CCT Pro	CCT Pro	GTG Val	GAC Asp	ACC Thr 340	AAA Lys	GCC Ala	GCA Ala	GAG Glu	AAG Lys 345	GAA Glu	1358		
AAG Lys	AAG Lys	CCA Pro	CCC Pro 350	ACA Thr	GCC Ala	ACC Thr	ACC Thr	AAG Lys 355	GGG Gly	AGA Arg	GGA Gly	AAA Lys	GGA Gly 360	AAA Lys	GGC Gly	1406		

AAG AAG AAA GGC AAA GTG AAA GAG GAA GTG GAG GAA GAG ACG GAC CCC Lys Lys Lys Gly Lys Val Lys Glu Glu Val Glu Glu Thr Asp Pro 365 370 375	1454
CGG AAG CTT GAG CTG CTC AAC TGG GTG AAT GCC CTG GAG CAA GCC ATG Arg Lys Leu Glu Leu Leu Asn Trp Val Asn Ala Leu Glu Gln Ala Met 380 385 390	1502
CTG GAT GCT CTT GTC CTA GAT CGG GTG GAC TTT GTA AAG CTC CTG ATT Leu Asp Ala Leu Val Leu Asp Arg Val Asp Phe Val Lys Leu Leu Ile 395 400 405 410	1550
GAA AAC GGA GTG AAC ATG CAG CAT TTC CTC ACC ATC CCG AGG CTG GAG Glu Asn Gly Val Asn Met Gln His Phe Leu Thr Ile Pro Arg Leu Glu 415 420 425	1598
GAG CTA TAC AAC ACC AGA CTG GGC CCA CCA AAC ACC CTT CAT CTG CTG Glu Leu Tyr Asn Thr Arg Leu Gly Pro Pro Asn Thr Leu His Leu Leu 430 435 440	1646
GTG CGG GAT GTA AAG AAG AGC AAC CTT CCA CCT GAT TAC CAC ATC AGC Val Arg Asp Val Lys Lys Ser Asn Leu Pro Pro Asp Tyr His Ile Ser 445 450 455	1694
CTC ATT GAT ATA GGA CTG GTG CTG GAG TAC CTC ATG GGC GGT GCC TAC Leu Ile Asp Ile Gly Leu Val Leu Glu Tyr Leu Met Gly Gly Ala Tyr 460 465 470	1742
CGC TGC AAC TAC ACT CGG AAA AGC TTC CGG ACT CTC TAC AAC AAC TTG Arg Cys Asn Tyr Thr Arg Lys Ser Phe Arg Thr Leu Tyr Asn Asn Leu 475 480 485 490	1790
TTT GGC CCT AAG AGG GTA GAG CTC AGC AGA CAC ACA GTG TCC TGT GCC Phe Gly Pro Lys Arg Val Glu Leu Ser Arg His Thr Val Ser Cys Ala 495 500 505	1838
TCC CAG AGT AAC ATG TGG TTC CTT GAT GTG CTT CCC CAA AAG CCC ACC Ser Gln Ser Asn Met Trp Phe Leu Asp Val Leu Pro Gln Lys Pro Thr 510 515 520	1886
TGT GCA GAA TGC AAC TCT TCA CCT CAC CTG TCC CAA ACT GAC ATC ACC Cys Ala Glu Cys Asn Ser Ser Pro His Leu Ser Gln Thr Asp Ile Thr 525 530 535	1934
CCA CCT CTG CCC T GACACCCAGT GCAGGGCCTC CTAGCTTTCA CATGCAGCCA Pro Pro Leu Pro 540	1987
TTACATCGC CTCTCAAGAC TGGGCCAGGC AGTGCAACCT GTCAAGCATG TCTGTCTCC	2047
CCTCCTTCCT ACAATAGCCC CCCCTCTGGG CCCCATGCCT CTGCTCTCTC AGCCCGTTCT	2107
CCTCCCCACT GATCACTGGC GCTCCTGTTG TCTTCCAAGG CAAGGAACAA GGAAAAGCAT	2167
CTTTTGGCCC ACAAAGTTT AGGGCTCCCC GCTGTTCAAC CATAGCCAAC CTCACTGTAC	2227
ATCGGAGTCA TCCAGGCCAG CTGCCACACA CAAGCCTTCC CCACCCTATC CCAATAGACC	2287

CTATTCCTCC ATCAAAATCA AAGCTAACTC CTGGCCTGCC ACATTGCTTC TTCTTGCTCC	2347
AGCCTGTAA ACCTCCAATA AATGTCAGAT CTGTGGGAA CCTTCCTCAC TCTCACTCCA	2407
CAGTTTGTAC AGAGAGCGAG AGCCTCGTTT GGTTCCTACTT ACAAGGAAGG CTTTGTGTCT	2467
GTCTGTCCTT CCCAACTGAC TTCTGTTGAC AGAAGCAGTT TCCACATGAA AGCGTTGACT	2527
CACCTGGATG TTGTCATTAA TTAATAGTGA TACAAAATAT TGACACTTCT TTTCCTGCTT	2587
CTTTGTTATG CAGCCGAAAG CACTTAAGCT TCTGGGAATG GAAGTAAGTA GGACATGTTT	2647
GTGGCAGTTT ATTTACTATA TATACCTTTG TCATTCTGTG GAAGCAAAAA TTGCAATGTT	2707
TTCCATGAAT AAAGCTCGTG CC	2729

(2) INFORMATION FOR SEQ ID NO:3:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Tyr	Ile	Arg	Val	Ser	Tyr	Asp	Thr	Lys	Pro	Asp	Ser	Leu	Leu	His
1				5					10					15	
Leu	Met	Val	Lys	Asp	Trp	Gln	Leu	Glu	Leu	Pro	Lys	Leu	Leu	Ile	Ser
		20					25						30		
Val	His	Gly	Gly	Leu	Gln	Ser	Phe	Glu	Met	Gln	Ser	Lys	Leu	Lys	Gln
		35				40						45			
Val	Phe	Gly	Lys	Gly	Leu	Ile	Lys	Ala	Ala	Met	Thr	Thr	Gly	Ala	Trp
	50					55					60				
Ile	Phe	Thr	Gly	Gly	Val	Ser	Thr	Gly	Val	Val	Ser	His	Val	Gly	Asp
65					70					75					80
Ala	Leu	Lys	Asp	His	Ser	Ser	Lys	Ser	Arg	Gly	Arg	Leu	Cys	Ala	Ile
				85					90					95	
Gly	Ile	Ala	Pro	Trp	Gly	Met	Val	Glu	Asn	Lys	Glu	Asp	Leu	Ile	Gly
		100						105					110		
Lys	Asp	Val	Thr	Arg	Val	Tyr	Gln	Thr	Met	Ser	Asn	Pro	Leu	Ser	Lys
		115					120					125			
Leu	Ser	Val	Leu	Asn	Asn	Ser	His	Thr	His	Phe	Ile	Leu	Ala	Asp	Asn
		130				135					140				
Gly	Thr	Leu	Gly	Lys	Tyr	Gly	Ala	Glu	Val	Lys	Leu	Arg	Arg	Gln	Leu
145					150					155					160
Glu	Lys	His	Ile	Ser	Leu	Gln	Lys	Ile	Asn	Thr	Arg	Leu	Gly	Gln	Gly
				165					170					175	

Val Pro Val Val Gly Leu Val Val Glu Gly Gly Pro Asn Val Val Ser
 180 185 190
 Ile Val Leu Glu Tyr Leu Lys Glu Asp Pro Pro Val Pro Val Val Val
 195 200 205
 Cys Asp Gly Ser Gly Arg Ala Ser Asp Ile Leu Ser Phe Ala His Lys
 210 215 220
 Tyr Cys Asp Glu Gly Gly Val Ile Asn Glu Ser Leu Arg Asp Gln Leu
 225 230 235 240
 Leu Val Thr Ile Gln Lys Thr Phe Asn Tyr Ser Lys Ser Gln Ser Tyr
 245 250 255
 Gln Leu Phe Ala Ile Ile Met Glu Cys Met Lys Lys Lys Glu Leu Val
 260 265 270
 Thr Val Phe Arg Met Gly Ser Glu Gly Gln Gln Asp Val Glu Met Ala
 275 280 285
 Ile Leu Thr Ala Leu Leu Lys Gly Thr Asn Ala Ser Ala Pro Asp Gln
 290 295 300
 Leu Ser Leu Ala Leu Ala Trp Asn Arg Val Asp Ile Ala Arg Ser Gln
 305 310 315 320
 Ile Phe Val Phe Gly Pro His Trp Pro Pro Leu Gly Ser Leu Ala Pro
 325 330 335
 Pro Val Asp Thr Lys Ala Ala Glu Lys Glu Lys Lys Pro Pro Thr Ala
 340 345 350
 Thr Thr Lys Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys Gly Lys Val
 355 360 365
 Lys Glu Glu Val Glu Glu Glu Thr Asp Pro Arg Lys Leu Glu Leu Leu
 370 375 380
 Asn Trp Val Asn Ala Leu Glu Gln Ala Met Leu Asp Ala Leu Val Leu
 385 390 395 400
 Asp Arg Val Asp Phe Val Lys Leu Leu Ile Glu Asn Gly Val Asn Met
 405 410 415
 Gln His Phe Leu Thr Ile Pro Arg Leu Glu Glu Leu Tyr Asn Thr Arg
 420 425 430
 Leu Gly Pro Pro Asn Thr Leu His Leu Leu Val Arg Asp Val Lys Lys
 435 440 445
 Ser Asn Leu Pro Pro Asp Tyr His Ile Ser Leu Ile Asp Ile Gly Leu
 450 455 460
 Val Leu Glu Tyr Leu Met Gly Gly Ala Tyr Arg Cys Asn Tyr Thr Arg
 465 470 475 480
 Lys Ser Phe Arg Thr Leu Tyr Asn Asn Leu Phe Gly Pro Lys Arg Val

	485		490		495										
Glu	Leu	Ser	Arg	His	Thr	Val	Ser	Cys	Ala	Ser	Gln	Ser	Asn	Met	Trp
			500					505					510		
Phe	Leu	Asp	Val	Leu	Pro	Gln	Lys	Pro	Thr	Cys	Ala	Glu	Cys	Asn	Ser
		515					520					525			
Ser	Pro	His	Leu	Ser	Gln	Thr	Asp	Ile	Thr	Pro	Pro	Leu	Pro		
	530					535					540				

(2) INFORMATION FOR SEQ ID NO:4:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGGGAAGCAC ATCAAGGAAC

20

(2) INFORMATION FOR SEQ ID NO:5:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCAACTACTA CACTCGGAAA AGC

23

(2) INFORMATION FOR SEQ ID NO:6:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4944 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 346..4837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ACTCATTATA GGGNTCGAGC GGCCGCCCGG GCAGGTTTGA GCTGTGCCCT CTCCATTCCA

60

CTGCTGTGGC AGGGTCAGAA ATCTTGATA GAGAAAACCT TTTGCAAACG GGAATGTATC

120

GAA TAC CTG CAA GAA GAG CCT CCC ATC CCT GTG GTG ATT TGT GAT GGC Glu Tyr Leu Gln Glu Glu Pro Pro Ile Pr Val Val Ile Cys Asp Gly 200 205 210	978
AGC GGA CGT GCC TCG GAC ATC CTG TCC TTT GCG CAC AAG TAC TGT GAA Ser Gly Arg Ala Ser Asp Ile Leu Ser Phe Ala His Lys Tyr Cys Glu 215 220 225	1026
GAA GGC GGA ATA ATA AAT GAG TCC CTC AGG GAG CAG CTT CTA GTT ACC Glu Gly Gly Ile Ile Asn Glu Ser Leu Arg Glu Gln Leu Leu Val Thr 230 235 240	1074
ATT CAG AAA ACA TTT AAT TAT AAT AAG GCA CAA TCA CAT CAG CTG TTT Ile Gln Lys Thr Phe Asn Tyr Asn Lys Ala Gln Ser His Gln Leu Phe 245 250 255	1122
GCA ATT ATA ATG GAG TGC ATG AAG AAG AAA GAA CTC GTC ACT GTG TTC Ala Ile Ile Met Glu Cys Met Lys Lys Lys Glu Leu Val Thr Val Phe 260 265 270 275	1170
AGA ATG GGT TCT GAG GGC CAG CAG GAC ATC GAG ATG GCA ATT TTA ACT Arg Met Gly Ser Glu Gly Gln Gln Asp Ile Glu Met Ala Ile Leu Thr 280 285 290	1218
GCC CTG CTG AAA GGA ACA AAC GTA TCT GCT CCA GAT CAG CTG AGC TTG Ala Leu Leu Lys Gly Thr Asn Val Ser Ala Pro Asp Gln Leu Ser Leu 295 300 305	1266
GCA CTG GCT TGG AAC CGC GTG GAC ATA GCA CGA AGC CAG ATC TTT GTC Ala Leu Ala Trp Asn Arg Val Asp Ile Ala Arg Ser Gln Ile Phe Val 310 315 320	1314
TTT GGG CCC CAC TGG ACG CCC CTG GGA AGC CTG GCA CCC CCG ACG GAC Phe Gly Pro His Trp Thr Pro Leu Gly Ser Leu Ala Pro Pro Thr Asp 325 330 335	1362
AGC AAA GCC ACG GAG AAG GAG AAG AAG CCA CCC ATG GCC ACC ACC AAG Ser Lys Ala Thr Glu Lys Glu Lys Lys Pro Pro Met Ala Thr Thr Lys 340 345 350 355	1410
GGA GGA AGA GGA AAA GGG AAA GGC AAG AAG AAA GGG AAA GTG AAA GAG Gly Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys Gly Lys Val Lys Glu 360 365 370	1458
GAA GTG GAG GAA GAA ACT GAC CCC CGG AAG ATA GAG CTG CTG AAC TGG Glu Val Glu Glu Glu Thr Asp Pro Arg Lys Ile Glu Leu Leu Asn Trp 375 380 385	1506
GTG AAT GCT TTG GAG CAA GCG ATG CTA GAT GCT TTA GTC TTA GAT CGT Val Asn Ala Leu Glu Gln Ala Met Leu Asp Ala Leu Val Leu Asp Arg 390 395 400	1554
GTC GAC TTT GTG AAG CTC CTG ATT GAA AAC GGA GTG AAC ATG CAA CAC Val Asp Phe Val Lys Leu Leu Ile Glu Asn Gly Val Asn Met Gln His 405 410 415	1602
TTT CTG ACC ATT CCG AGG CTG GAG GAG CTT TAT AAC ACA AGA CTG GGT Phe Leu Thr Ile Pro Arg Leu Glu Glu Leu Tyr Asn Thr Arg Leu Gly	1650

420				425				430				435				
CCA Pr	CCA Pr	AAC Asn	ACA Thr	CTT Leu 440	CAT His	CTG Leu	CTG Leu	GTG Val	AGG Arg 445	GAT Asp	GTG Val	AAA Lys	AA Lys	AGC Ser 450	AAC Asn	1698
CTT Leu	CCG Pro	CCT Pro	GAT Asp 455	TAC Tyr	CAC His	ATC Ile	AGC Ser	CTC Leu 460	ATA Ile	GAC Asp	ATC Ile	GGG Gly	CTC Leu 465	GTG Val	CTG Leu	1746
GAG Glu	TAC Tyr	CTC Leu 470	ATG Met	GGA Gly	GGA Gly	GCC Ala	TAC Tyr 475	CGC Arg	TGC Cys	AAC Asn	TAC Tyr	ACT Thr 480	CGG Arg	AAA Lys	AAC Asn	1794
TTT Phe	CGG Arg 485	ACC Thr	CTT Leu	TAC Tyr	AAC Asn	AAC Asn 490	TTG Leu	TTT Phe	GGA Gly	CCA Pro	AAG Lys 495	AGG Arg	CCT Pro	AAA Lys	GCT Ala	1842
CTT Leu 500	AAA Lys	CTT Leu	CTG Leu	GGA Gly 505	ATG Met	GAA Glu	GAT Asp	GAT Asp	GAG Glu	CCT Pro 510	CCA Pro	GCT Ala	AAA Lys	GGG Gly	AAG Lys 515	1890
AAA Lys	AAA Lys	AAA Lys	AAA Lys	AAG Lys 520	AAA Lys	AAG Lys	GAG Glu	GAA Glu	GAG Glu 525	ATC Ile	GAC Asp	ATT Ile	GAT Asp	GTG Val 530	GAC Asp	1938
GAC Asp	CCT Pro	GCC Ala	GTG Val 535	AGT Ser	CGG Arg	TTC Phe	CAG Gln	TAT Tyr 540	CCC Pro	TTC Phe	CAC His	GAG Glu	CTG Leu 545	ATG Met	GTG Val	1986
TGG Trp	GCA Ala	GTG Val 550	CTG Leu	ATG Met	AAA Lys	CGC Arg	CAG Gln 555	AAA Lys	ATG Met	GCA Ala	GTG Val	TTC Phe 560	CTC Leu	TGG Trp	CAG Gln	2034
CGA Arg	GGG Gly 565	GAA Glu	GAG Glu	AGC Ser	ATG Met	GCC Ala 570	AAG Lys	GCC Ala	CTG Leu	GTG Val	GCC Ala 575	TGC Cys	AAG Lys	CTC Leu	TAC Tyr	2082
AAG Lys 580	GCC Ala	ATG Met	GCC Ala	CAC His	GAG Glu 585	TCC Ser	TCC Ser	GAG Glu	AGT Ser	GAT Asp 590	CTG Leu	GTG Val	GAT Asp	GAC Asp	ATC Ile 595	2130
TCC Ser	CAG Gln	GAC Asp	TTG Leu 600	GAT Asp	AAC Asn	AAT Asn	TCC Ser	AAA Lys	GAC Asp 605	TTC Phe	GGC Gly	CAG Gln	CTT Leu 610	GCT Ala	TTG Leu	2178
GAG Glu	TTA Leu	TTA Leu	GAC Asp 615	CAG Gln	TCC Ser	TAT Tyr	AAG Lys	CAT His 620	GAC Asp	GAG Glu	CAG Gln	ATC Ile	GCT Ala 625	ATG Met	AAA Lys	2226
CTC Leu	CTG Leu	ACC Thr 630	TAC Tyr	GAG Glu	CTG Leu	AAA Lys	AAC Asn 635	TGG Trp	AGC Ser	AAC Asn	TCG Ser	ACC Thr 640	TGC Cys	CTC Leu	AAA Lys	2274
CTG Leu	GCC Ala 645	GTG Val	GCA Ala	GCC Ala	AAA Lys	CAC His 650	CGG Arg	GAC Asp	TTC Phe	ATT Ile	GCT Ala 655	CAC His	ACC Thr	TGC Cys	AGC Ser	2322

CAG Gln 660	ATG Met	CTG Leu	CTG Leu	ACC Thr	GAT Asp 665	ATG Met	TGG Trp	ATG Met	GGA Gly 670	AGA Arg	CTG Leu	CGG Arg	ATG Met	CGG Arg	AAG Lys 675	2370
AAC Asn	CCC Pro	GGC Gly	CTG Leu	AAG Lys 680	GTT Val	ATC Ile	ATG Met	GGG Gly	ATT Ile 685	CTT Leu	CTA Leu	CCC Pro	CCC Pro	ACC Thr 690	ATC Ile	2418
TTG Leu	TTT Phe	TTG Leu	GAA Glu 695	TTT Phe	CGC Arg	ACA Thr	TAT Tyr	GAT Asp 700	GAT Asp	TTC Phe	TCG Ser	TAT Tyr	CAA Gln 705	ACA Thr	TCC Ser	2466
AAG Lys	GAA Glu	AAC Asn 710	GAG Glu	GAT Asp	GGC Gly	AAA Lys	GAA Glu 715	AAA Lys	GAA Glu	GAG Glu	GAA Glu	AAT Asn 720	ACG Thr	GAT Asp	GCA Ala	2514
AAT Asn 725	GCA Ala	GAT Asp	GCT Ala	GGC Gly	TCA Ser	AGA Arg 730	AAG Lys	GGG Gly	GAT Asp	GAG Glu	GAG Glu	AAC Asn 735	GAG Glu	CAT His	AAA Lys	2562
AAA Lys 740	CAG Gln	AGA Arg	ATT Ile	ATC Ile	CCC Pro 745	ATC Ile	GGA Gly	ACA Thr	AAA Lys	ATC Ile 750	TGT Cys	AAA Lys	TTC Phe	TAT Tyr	AAC Asn 755	2610
GCG Ala	CCC Pro	ATT Ile	GTC Val	AAG Lys 760	TTC Phe	TGG Trp	TTT Phe	TAC Tyr 765	ACA Thr	ATA Ile	TCA Ser	TAC Tyr	TTG Leu	GGC Gly 770	TAC Tyr	2658
CTG Leu	CTG Leu	CTG Leu	TTT Phe 775	AAC Asn	TAC Tyr	GTC Val	ATC Ile	CTG Leu 780	GTG Val	CGG Arg	ATG Met	GAT Asp	GGC Gly 785	TGG Trp	CCG Pro	2706
TCC Ser	CTC Leu	CAG Gln 790	GAG Glu	TGG Trp	ATC Ile	GTC Val	ATC Ile	TCC Ser 795	TAC Tyr	ATC Ile	GTG Val	AGC Ser	CTG Leu	GCG Ala	TTA Leu	2754
GAG Glu 805	AAG Lys	ATA Ile	CGA Arg	GAG Glu	ATC Ile	CTC Leu 810	ATG Met	TCA Ser	GAA Glu	CCA Pro	GGC Gly 815	AAA Lys	CTC Leu	AGC Ser	CAG Gln	2802
AAA Lys 820	ATC Ile	AAA Lys	GTT Val	TGG Trp	CTT Leu 825	CAG Gln	GAG Glu	TAC Tyr	TGG Trp	AAC Asn 830	ATC Ile	ACA Thr	GAT Asp	CTC Leu	GTG Val 835	2850
GCC Ala	ATT Ile	TCC Ser	ACA Thr 840	TTC Phe	ATG Met	ATT Ile	GGA Gly	GCA Ala 845	ATG Met	GCC Ala	ACG Thr	AGA Arg	TCT Ser	GTG Val 850	ATG Met	2898
ATG Met	ATT Ile	GGA Gly 855	AAG Lys	ATG Met	ATG Met	ATC Ile	GAC Asp	ATG Met 860	CTG Leu	TAC Tyr	TTT Phe	GTG Val	GTC Val 865	ATC Ile	ATG Met	2946
CTG Leu	GTC Val	GTG Val 870	CTC Leu	ATG Met	AGT Ser	TTC Phe	GGA Gly 875	GTA Val	GCC Ala	CGT Arg	CAA Gln	GCC Ala 880	ATT Ile	CTG Leu	CAT His	2994
CCA Pro	GAG Glu	GAG Glu	AAG Lys	CCC Pro	TCT Ser	TGG Trp	AAA Lys	CTG Leu	GCC Ala	CGA Arg	AAC Asn	ATC Ile	TTC Phe	TAC Tyr	ATG Met	3042

885	890	895	
CCC TAC TGG ATG ATC TAT GGA GAG GTG TTT GCA GAC CAG ATA GAC CTC Pr Tyr Trp Met Ile Tyr Gly Glu Val Phe Ala Asp Gln Ile Asp Leu 900 905 910 915			3090
TAC GCC ATG GAA ATT AAT CCT CCT TGT GGT GAG AAC CTA TAT GAT GAG Tyr Ala Met Glu Ile Asn Pro Pro Cys Gly Glu Asn Leu Tyr Asp Glu 920 925 930			3138
GAG GGC AAG CGG CTT CCT CCC TGT ATC CCC GGC GCC TGG CTC ACT CCA Glu Gly Lys Arg Leu Pro Pro Cys Ile Pro Gly Ala Trp Leu Thr Pro 935 940 945			3186
GCA CTC ATG GCG TGC TAT CTA CTG GTC GCC AAC ATC CTG CTG GTG AAC Ala Leu Met Ala Cys Tyr Leu Leu Val Ala Asn Ile Leu Leu Val Asn 950 955 960			3234
CTG CTG ATT GCT GTG TTC AAC AAT ACC TTC TTT GAA GTA AAA TCA ATA Leu Leu Ile Ala Val Phe Asn Asn Thr Phe Phe Glu Val Lys Ser Ile 965 970 975			3282
TCC AAC CAG GTG TGG AAG TTC CAG CGA TAT CAG CTG ATT ATG ACA TTT Ser Asn Gln Val Trp Lys Phe Gln Arg Tyr Gln Leu Ile Met Thr Phe 980 985 990 995			3330
CAT GAC AGG CCA GTC CTG CCC CCA CCG ATG ATC ATT TTA AGC CAC ATC His Asp Arg Pro Val Leu Pro Pro Met Ile Ile Leu Ser His Ile 1000 1005 1010			3378
TAC ATC ATC ATT ATG CGT CTC AGC GGC CGC TGC AGG AAA AAG AGA GAA Tyr Ile Ile Ile Met Arg Leu Ser Gly Arg Cys Arg Lys Lys Arg Glu 1015 1020 1025			3426
GGG GAC CAA GAG GAA CGG GAT CGT GGA TTG AAG CTC TTC CTT AGC GAC Gly Asp Gln Glu Glu Arg Asp Arg Gly Leu Lys Leu Phe Leu Ser Asp 1030 1035 1040			3474
GAG GAG CTA AAG AGG CTG CAT GAG TTC GAG GAG CAG TGC GTG CAG GAG Glu Glu Leu Lys Arg Leu His Glu Phe Glu Glu Gln Cys Val Gln Glu 1045 1050 1055			3522
CAC TTC CGG GAG AAG GAG GAT GAG CAG CAG TCG TCC AGC GAC GAG CGC His Phe Arg Glu Lys Glu Asp Glu Gln Gln Ser Ser Ser Asp Glu Arg 1060 1065 1070 1075			3570
ATC CGG GTC ACT TCT GAA AGA GTT GAA AAT ATG TCA ATG AGG TTG GAA Ile Arg Val Thr Ser Glu Arg Val Glu Asn Met Ser Met Arg Leu Glu 1080 1085 1090			3618
GAA ATC AAT GAA AGA GAA ACT TTT ATG AAA ACT TCC CTG CAG ACT GTT Glu Ile Asn Glu Arg Glu Thr Phe Met Lys Thr Ser Leu Gln Thr Val 1095 1100 1105			3666
GAC CTT CGA CTT GCT CAG CTA GAA GAA TTA TCT AAC AGA ATG GTG AAT Asp Leu Arg Leu Ala Gln Leu Glu Glu Leu Ser Asn Arg Met Val Asn 1110 1115 1120			3714

GCT CTT GAA AAT CTT GCG GGA ATC GAC AGG TCT GAC CTG ATC CAG GCA Ala Leu Glu Asn Leu Ala Gly Ile Asp Arg Ser Asp Leu Ile Gln Ala 1125 1130 1135	3762
CGG TCC CGG GCT TCT TCT GAA TGT GAG GCA ACG TAT CTT CTC CGG CAA Arg Ser Arg Ala Ser Ser Glu Cys Glu Ala Thr Tyr Leu Leu Arg Gln 1140 1145 1150 1155	3810
AGC AGC ATC AAT AGC GCT GAT GGC TAC AGC TTG TAT CGA TAT CAT TTT Ser Ser Ile Asn Ser Ala Asp Gly Tyr Ser Leu Tyr Arg Tyr His Phe 1160 1165 1170	3858
AAC GGA GAA GAG TTA TTA TTT GAG GAT ACA TCT CTC TCC ACG TCA CCA Asn Gly Glu Glu Leu Leu Phe Glu Asp Thr Ser Leu Ser Thr Ser Pro 1175 1180 1185	3906
GGG ACA GGA GTC AGG AAA AAA ACC TGT TCC TTC CGT ATA AAG GAA GAG Gly Thr Gly Val Arg Lys Lys Thr Cys Ser Phe Arg Ile Lys Glu Glu 1190 1195 1200	3954
AAG GAC GTG AAA ACG CAC CTA GTC CCA GAA TGT CAG AAC AGT CTT CAC Lys Asp Val Lys Thr His Leu Val Pro Glu Cys Gln Asn Ser Leu His 1205 1210 1215	4002
CTT TCA CTG GGC ACA AGC ACA TCA GCA ACC CCA GAT GGC AGT CAC CTT Leu Ser Leu Gly Thr Ser Thr Ser Ala Thr Pro Asp Gly Ser His Leu 1220 1225 1230 1235	4050
GCA GTA GAT GAC TTA AAG AAC GCT GAA GAG TCA AAA TTA GGT CCA GAT Ala Val Asp Asp Leu Lys Asn Ala Glu Glu Ser Lys Leu Gly Pro Asp 1240 1245 1250	4098
ATT GGG ATT TCA AAG GAA GAT GAT GAA AGA CAG ACA GAC TCT AAA AAA Ile Gly Ile Ser Lys Glu Asp Asp Glu Arg Gln Thr Asp Ser Lys Lys 1255 1260 1265	4146
GAA GAA ACT ATT TCC CCA AGT TTA AAT AAA ACA GAT GTG ATA CAT GGA Glu Glu Thr Ile Ser Pro Ser Leu Asn Lys Thr Asp Val Ile His Gly 1270 1275 1280	4194
CAG GAC AAA TCA GAT GTT CAA AAC ACT CAG CTA ACA GTG GAA ACG ACA Gln Asp Lys Ser Asp Val Gln Asn Thr Gln Leu Thr Val Glu Thr Thr 1285 1290 1295	4242
AAT ATA GAA GGC ACT ATT TCC TAT CCC CTG GAA GAA ACC AAA ATT ACA Asn Ile Glu Gly Thr Ile Ser Tyr Pro Leu Glu Glu Thr Lys Ile Thr 1300 1305 1310 1315	4290
CGC TAT TTC CCC GAT GAA ACG ATC AAT GCT TGT AAA ACA ATG AAG TCC Arg Tyr Phe Pro Asp Glu Thr Ile Asn Ala Cys Lys Thr Met Lys Ser 1320 1325 1330	4338
AGA AGC TTC GTC TAT TCC CGG GGA AGA AAG CTG GTC GGT GGG GTT AAC Arg Ser Phe Val Tyr Ser Arg Gly Arg Lys Leu Val Gly Gly Val Asn 1335 1340 1345	4386
CAG GAT GTA GAG TAC AGT TCA ATC ACG GAC CAG CAA TTG ACG ACG GAA Gln Asp Val Glu Tyr Ser Ser Ile Thr Asp Gln Gln Leu Thr Thr Glu 1350 1355 1360	4434

1350	1355	1360	
TGG CAA TGC CAA GTT CAA AAG ATC ACG CGC TCT CAT AGC ACA GAT ATT Trp Gln Cys Gln Val Gln Lys Ile Thr Arg Ser His Ser Thr Asp Ile 1365 1370 1375			4482
CCT TAC ATT GTG TCG GAA GCT GCA GTG CAA GCT GAG CAA AAA GAG CAG Pro Tyr Ile Val Ser Glu Ala Ala Val Gln Ala Glu Gln Lys Glu Gln 1380 1385 1390 1395			4530
TTT GCA GAT ATG CAA GAT GAA CAC CAT GTC GCT GAA GCA ATT CCT CGA Phe Ala Asp Met Gln Asp Glu His His Val Ala Glu Ala Ile Pro Arg 1400 1405 1410			4578
ATC CCT CGC TTG TCC CTA ACC ATT ACT GAC AGA AAT GGG ATG GAA AAC Ile Pro Arg Leu Ser Leu Thr Ile Thr Asp Arg Asn Gly Met Glu Asn 1415 1420 1425			4626
TTA CTG TCT GTG AAG CCA GAT CAA ACT TTG GGA TTC CCA TCT CTC AGG Leu Leu Ser Val Lys Pro Asp Gln Thr Leu Gly Phe Pro Ser Leu Arg 1430 1435 1440			4674
TCA AAA AGT TTA CAT GGA CAT CCT AGG AAT GTG AAA TCC ATT CAG GGA Ser Lys Ser Leu His Gly His Pro Arg Asn Val Lys Ser Ile Gln Gly 1445 1450 1455			4722
AAG TTA GAC AGA TCT GGA CAT GCC AGT AGT GTA AGC AGC TTA GTA ATT Lys Leu Asp Arg Ser Gly His Ala Ser Ser Val Ser Ser Leu Val Ile 1460 1465 1470 1475			4770
GTG TCT GGA ATG ACA GCA GAA GAA AAA AAG GTT AAG AAA GAG AAA GCT Val Ser Gly Met Thr Ala Glu Glu Lys Lys Val Lys Lys Glu Lys Ala 1480 1485 1490			4818
TCC ACA GAA ACT GAA TGC T AGTCTGTTTT GTTCTTTTAA TTTTTTTTTT Ser Thr Glu Thr Glu Cys 1495			4867
TAACAGTCAG AACCACTAAT GGGTGTGATC TTGGCCATCC TAAACATCCA TCCAATTTCC			4927
TAAAAACATT TTCCCTT			4944

(2) INFORMATION FOR SEQ ID NO:7:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1497 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Tyr	Ile	Arg	Val	Ser	Tyr	Asp	Thr	Lys	Pro	Asp	Ser	Leu	Leu	His
1				5					10					15	
Leu	Met	Val	Lys	Asp	Trp	Gln	Leu	Glu	Leu	Pro	Lys	Leu	Leu	Ile	Ser
		20						25					30		
Val	His	Gly	Gly	Leu	Gln	Asn	Phe	Glu	Met	Gln	Pro	Lys	Leu	Lys	Gln

35					40					45					
Val	Phe	Gly	Lys	Gly	Leu	Ile	Lys	Ala	Ala	Met	Thr	Thr	Gly	Ala	Trp
50						55					60				
Ile	Phe	Thr	Gly	Gly	Val	Ser	Thr	Gly	Val	Ile	Ser	His	Val	Gly	Asp
65					70					75					80
Ala	Leu	Lys	Asp	His	Ser	Ser	Lys	Ser	Arg	Gly	Arg	Val	Cys	Ala	Ile
				85					90					95	
Gly	Ile	Ala	Pro	Trp	Gly	Ile	Val	Glu	Asn	Lys	Glu	Asp	Leu	Val	Gly
			100					105					110		
Lys	Asp	Val	Thr	Arg	Val	Tyr	Gln	Thr	Met	Ser	Asn	Pro	Leu	Ser	Lys
		115					120					125			
Leu	Ser	Val	Leu	Asn	Asn	Ser	His	Thr	His	Phe	Ile	Leu	Ala	Asp	Asn
	130					135					140				
Gly	Thr	Leu	Gly	Lys	Tyr	Gly	Ala	Glu	Val	Lys	Leu	Arg	Arg	Leu	Leu
145				150						155					160
Glu	Lys	His	Ile	Ser	Leu	Gln	Lys	Ile	Asn	Thr	Arg	Leu	Gly	Gln	Gly
				165					170					175	
Val	Pro	Leu	Val	Gly	Leu	Val	Val	Glu	Gly	Gly	Pro	Asn	Val	Val	Ser
			180					185					190		
Ile	Val	Leu	Glu	Tyr	Leu	Gln	Glu	Glu	Pro	Pro	Ile	Pro	Val	Val	Ile
		195					200					205			
Cys	Asp	Gly	Ser	Gly	Arg	Ala	Ser	Asp	Ile	Leu	Ser	Phe	Ala	His	Lys
	210					215					220				
Tyr	Cys	Glu	Glu	Gly	Gly	Ile	Ile	Asn	Glu	Ser	Leu	Arg	Glu	Gln	Leu
225				230					235						240
Leu	Val	Thr	Ile	Gln	Lys	Thr	Phe	Asn	Tyr	Asn	Lys	Ala	Gln	Ser	His
				245				250						255	
Gln	Leu	Phe	Ala	Ile	Ile	Met	Glu	Cys	Met	Lys	Lys	Lys	Glu	Leu	Val
		260					265						270		
Thr	Val	Phe	Arg	Met	Gly	Ser	Glu	Gly	Gln	Gln	Asp	Ile	Glu	Met	Ala
		275					280					285			
Ile	Leu	Thr	Ala	Leu	Leu	Lys	Gly	Thr	Asn	Val	Ser	Ala	Pro	Asp	Gln
	290					295					300				
Leu	Ser	Leu	Ala	Leu	Ala	Trp	Asn	Arg	Val	Asp	Ile	Ala	Arg	Ser	Gln
305				310						315					320
Ile	Phe	Val	Phe	Gly	Pro	His	Trp	Thr	Pro	Leu	Gly	Ser	Leu	Ala	Pro
			325						330					335	
Pro	Thr	Asp	Ser	Lys	Ala	Thr	Glu	Lys	Glu	Lys	Lys	Pro	Pro	Met	Ala
			340				345						350		

Thr Thr Lys Gly Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys Gly Lys
 355 360 365
 Val Lys Glu Glu Val Glu Glu Glu Thr Asp Pro Arg Lys Ile Glu Leu
 370 375 380
 Leu Asn Trp Val Asn Ala Leu Glu Gln Ala Met Leu Asp Ala Leu Val
 385 390 395 400
 Leu Asp Arg Val Asp Phe Val Lys Leu Leu Ile Glu Asn Gly Val Asn
 405 410 415
 Met Gln His Phe Leu Thr Ile Pro Arg Leu Glu Glu Leu Tyr Asn Thr
 420 425 430
 Arg Leu Gly Pro Pro Asn Thr Leu His Leu Leu Val Arg Asp Val Lys
 435 440 445
 Lys Ser Asn Leu Pro Pro Asp Tyr His Ile Ser Leu Ile Asp Ile Gly
 450 455 460
 Leu Val Leu Glu Tyr Leu Met Gly Gly Ala Tyr Arg Cys Asn Tyr Thr
 465 470 475 480
 Arg Lys Asn Phe Arg Thr Leu Tyr Asn Asn Leu Phe Gly Pro Lys Arg
 485 490 495
 Pro Lys Ala Leu Lys Leu Leu Gly Met Glu Asp Asp Glu Pro Pro Ala
 500 505 510
 Lys Gly Lys Lys Lys Lys Lys Lys Lys Lys Glu Glu Glu Ile Asp Ile
 515 520 525
 Asp Val Asp Asp Pro Ala Val Ser Arg Phe Gln Tyr Pro Phe His Glu
 530 535 540
 Leu Met Val Trp Ala Val Leu Met Lys Arg Gln Lys Met Ala Val Phe
 545 550 555 560
 Leu Trp Gln Arg Gly Glu Glu Ser Met Ala Lys Ala Leu Val Ala Cys
 565 570 575
 Lys Leu Tyr Lys Ala Met Ala His Glu Ser Ser Glu Ser Asp Leu Val
 580 585 590
 Asp Asp Ile Ser Gln Asp Leu Asp Asn Asn Ser Lys Asp Phe Gly Gln
 595 600 605
 Leu Ala Leu Glu Leu Leu Asp Gln Ser Tyr Lys His Asp Glu Gln Ile
 610 615 620
 Ala Met Lys Leu Leu Thr Tyr Glu Leu Lys Asn Trp Ser Asn Ser Thr
 625 630 635 640
 Cys Leu Lys Leu Ala Val Ala Ala Lys His Arg Asp Phe Ile Ala His
 645 650 655

Thr Cys Ser Gln Met Leu Leu Thr Asp Met Trp Met Gly Arg Leu Arg
 660 665 670
 Met Arg Lys Asn Pro Gly Leu Lys Val Ile Met Gly Il Leu Leu Pro
 675 680 685
 Pro Thr Ile Leu Phe Leu Glu Phe Arg Thr Tyr Asp Asp Phe Ser Tyr
 690 695 700
 Gln Thr Ser Lys Glu Asn Glu Asp Gly Lys Glu Lys Glu Glu Glu Asn
 705 710 715 720
 Thr Asp Ala Asn Ala Asp Ala Gly Ser Arg Lys Gly Asp Glu Glu Asn
 725 730 735
 Glu His Lys Lys Gln Arg Ile Ile Pro Ile Gly Thr Lys Ile Cys Lys
 740 745 750
 Phe Tyr Asn Ala Pro Ile Val Lys Phe Trp Phe Tyr Thr Ile Ser Tyr
 755 760 765
 Leu Gly Tyr Leu Leu Leu Phe Asn Tyr Val Ile Leu Val Arg Met Asp
 770 775 780
 Gly Trp Pro Ser Leu Gln Glu Trp Ile Val Ile Ser Tyr Ile Val Ser
 785 790 795 800
 Leu Ala Leu Glu Lys Ile Arg Glu Ile Leu Met Ser Glu Pro Gly Lys
 805 810 815
 Leu Ser Gln Lys Ile Lys Val Trp Leu Gln Glu Tyr Trp Asn Ile Thr
 820 825 830
 Asp Leu Val Ala Ile Ser Thr Phe Met Ile Gly Ala Met Ala Thr Arg
 835 840 845
 Ser Val Met Met Ile Gly Lys Met Met Ile Asp Met Leu Tyr Phe Val
 850 855 860
 Val Ile Met Leu Val Val Leu Met Ser Phe Gly Val Ala Arg Gln Ala
 865 870 875 880
 Ile Leu His Pro Glu Glu Lys Pro Ser Trp Lys Leu Ala Arg Asn Ile
 885 890 895
 Phe Tyr Met Pro Tyr Trp Met Ile Tyr Gly Glu Val Phe Ala Asp Gln
 900 905 910
 Ile Asp Leu Tyr Ala Met Glu Ile Asn Pro Pro Cys Gly Glu Asn Leu
 915 920 925
 Tyr Asp Glu Glu Gly Lys Arg Leu Pro Pro Cys Ile Pro Gly Ala Trp
 930 935 940
 Leu Thr Pro Ala Leu Met Ala Cys Tyr Leu Leu Val Ala Asn Ile Leu
 945 950 955 960

Leu Val Asn Leu Leu Ile Ala Val Phe Asn Asn Thr Phe Phe Glu Val
 965 970 975
 Lys Ser Ile Ser Asn Gln Val Trp Lys Phe Gln Arg Tyr Gln Leu Ile
 980 985 990
 Met Thr Phe His Asp Arg Pro Val Leu Pro Pro Pro Met Ile Ile Leu
 995 1000 1005
 Ser His Ile Tyr Ile Ile Ile Met Arg Leu Ser Gly Arg Cys Arg Lys
 1010 1015 1020
 Lys Arg Glu Gly Asp Gln Glu Glu Arg Asp Arg Gly Leu Lys Leu Phe
 1025 1030 1035 1040
 Leu Ser Asp Glu Glu Leu Lys Arg Leu His Glu Phe Glu Glu Gln Cys
 1045 1050 1055
 Val Gln Glu His Phe Arg Glu Lys Glu Asp Glu Gln Gln Ser Ser Ser
 1060 1065 1070
 Asp Glu Arg Ile Arg Val Thr Ser Glu Arg Val Glu Asn Met Ser Met
 1075 1080 1085
 Arg Leu Glu Glu Ile Asn Glu Arg Glu Thr Phe Met Lys Thr Ser Leu
 1090 1095 1100
 Gln Thr Val Asp Leu Arg Leu Ala Gln Leu Glu Glu Leu Ser Asn Arg
 1105 1110 1115 1120
 Met Val Asn Ala Leu Glu Asn Leu Ala Gly Ile Asp Arg Ser Asp Leu
 1125 1130 1135
 Ile Gln Ala Arg Ser Arg Ala Ser Ser Glu Cys Glu Ala Thr Tyr Leu
 1140 1145 1150
 Leu Arg Gln Ser Ser Ile Asn Ser Ala Asp Gly Tyr Ser Leu Tyr Arg
 1155 1160 1165
 Tyr His Phe Asn Gly Glu Glu Leu Leu Phe Glu Asp Thr Ser Leu Ser
 1170 1175 1180
 Thr Ser Pro Gly Thr Gly Val Arg Lys Lys Thr Cys Ser Phe Arg Ile
 1185 1190 1195 1200
 Lys Glu Glu Lys Asp Val Lys Thr His Leu Val Pro Glu Cys Gln Asn
 1205 1210 1215
 Ser Leu His Leu Ser Leu Gly Thr Ser Thr Ser Ala Thr Pro Asp Gly
 1220 1225 1230
 Ser His Leu Ala Val Asp Asp Leu Lys Asn Ala Glu Glu Ser Lys Leu
 1235 1240 1245
 Gly Pro Asp Ile Gly Ile Ser Lys Glu Asp Asp Glu Arg Gln Thr Asp
 1250 1255 1260

Ser Lys Lys Glu Glu Thr Ile S r Pro Ser Leu Asn Lys Thr Asp Val
 1265 1270 1275 1280
 Ile His Gly Gln Asp Lys Ser Asp Val Gln Asn Thr Gln Leu Thr Val
 1285 1290 1295
 Glu Thr Thr Asn Ile Glu Gly Thr Ile Ser Tyr Pro Leu Glu Glu Thr
 1300 1305 1310
 Lys Ile Thr Arg Tyr Phe Pro Asp Glu Thr Ile Asn Ala Cys Lys Thr
 1315 1320 1325
 Met Lys Ser Arg Ser Phe Val Tyr Ser Arg Gly Arg Lys Leu Val Gly
 1330 1335 1340
 Gly Val Asn Gln Asp Val Glu Tyr Ser Ser Ile Thr Asp Gln Gln Leu
 1345 1350 1355 1360
 Thr Thr Glu Trp Gln Cys Gln Val Gln Lys Ile Thr Arg Ser His Ser
 1365 1370 1375
 Thr Asp Ile Pro Tyr Ile Val Ser Glu Ala Ala Val Gln Ala Glu Gln
 1380 1385 1390
 Lys Glu Gln Phe Ala Asp Met Gln Asp Glu His His Val Ala Glu Ala
 1395 1400 1405
 Ile Pro Arg Ile Pro Arg Leu Ser Leu Thr Ile Thr Asp Arg Asn Gly
 1410 1415 1420
 Met Glu Asn Leu Leu Ser Val Lys Pro Asp Gln Thr Leu Gly Phe Pro
 1425 1430 1435 1440
 Ser Leu Arg Ser Lys Ser Leu His Gly His Pro Arg Asn Val Lys Ser
 1445 1450 1455
 Ile Gln Gly Lys Leu Asp Arg Ser Gly His Ala Ser Ser Val Ser Ser
 1460 1465 1470
 Leu Val Ile Val Ser Gly Met Thr Ala Glu Glu Lys Lys Val Lys Lys
 1475 1480 1485
 Glu Lys Ala Ser Thr Glu Thr Glu Cys
 1490 1495

(2) INFORMATION FOR SEQ ID NO:8:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5055 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: DNA

(1x) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 346..4945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ACTCATTATA GGGNTCGAGC GGCCGCCCGG GCAGGTTTGA GCTGTGCCCT CTCCATTCCA	60
CTGCTGTGGC AGGGTCAGAA ATCTTGGATA GAGAAAACCT TTTGCAAACG GGAATGTATC	120
TTTGTAATTC CTAGCACGAA AGACTCTAAC AGGTGTTGCT GTGGCCAGTT CACCAACCAG	180
CATATCCCCC CTCTGCCAAG TGCAACACCC AGCAAAAATG AAGAGGAAAG CAAACAGGTG	240
GAGACTCAGC CTGAGAAATG GTCTGTTGCC AAGCACACCC AGAGCTACCC AACAGATTCC	300
TATGGAGTTC TTGAATTCCA GGGTGGCGGA TATTCCAATA AAGCC ATG TAT ATC	354
Met Tyr Ile	
1	
CGT GTA TCC TAT GAC ACC AAG CCA GAC TCA CTG CTC CAT CTC ATG GTG	402
Arg Val Ser Tyr Asp Thr Lys Pro Asp Ser Leu Leu His Leu Met Val	
5 10 15	
AAA GAT TGG CAG CTG GAA CTC CCC AAG CTC TTA ATA TCT GTG CAT GGA	450
Lys Asp Trp Gln Leu Glu Leu Pro Lys Leu Leu Ile Ser Val His Gly	
20 25 30 35	
GGC CTC CAG AAC TTT GAG ATG CAG CCC AAG CTG AAA CAA GTC TTT GGG	498
Gly Leu Gln Asn Phe Glu Met Gln Pro Lys Leu Lys Gln Val Phe Gly	
40 45 50	
AAA GGC CTG ATC AAG GCT GCT ATG ACC ACC GGG GCC TGG ATC TTC ACC	546
Lys Gly Leu Ile Lys Ala Ala Met Thr Thr Gly Ala Trp Ile Phe Thr	
55 60 65	
GGG GGT GTC AGC ACA GGT GTT ATC AGC CAC GTA GGG GAT GCC TTG AAA	594
Gly Gly Val Ser Thr Gly Val Ile Ser His Val Gly Asp Ala Leu Lys	
70 75 80	
GAC CAC TCC TCC AAG TCC AGA GGC CGG GTT TGT GCT ATA GGA ATT GCT	642
Asp His Ser Ser Lys Ser Arg Gly Arg Val Cys Ala Ile Gly Ile Ala	
85 90 95	
CCA TGG GGC ATC GTG GAG AAT AAG GAA GAC CTG GTT GGA AAG GAT GTA	690
Pro Trp Gly Ile Val Glu Asn Lys Glu Asp Leu Val Gly Lys Asp Val	
100 105 110 115	
ACA AGA GTG TAC CAG ACC ATG TCC AAC CCT CTA AGT AAG CTC TCT GTG	738
Thr Arg Val Tyr Gln Thr Met Ser Asn Pro Leu Ser Lys Leu Ser Val	
120 125 130	
CTC AAC AAC TCC CAC ACC CAC TTC ATC CTG GCT GAC AAT GGC ACC CTG	786
Leu Asn Asn Ser His Thr His Phe Ile Leu Ala Asp Asn Gly Thr Leu	
135 140 145	
GGC AAG TAT GGC GCC GAG GTG AAG CTG CGA AGG CTG CTG GAA AAG CAC	834

Gly	Lys	Tyr	Gly	Ala	Glu	Val	Lys	Leu	Arg	Arg	Leu	Leu	Glu	Lys	His	
		150					155					160				
ATC	TCC	CTC	CAG	AAG	ATC	AAC	ACA	AGA	CTG	GGG	CAG	GGC	GTG	CCC	CTC	882
Ile	Ser	Leu	Gln	Lys	Ile	Asn	Thr	Arg	Leu	Gly	Gln	Gly	Val	Pr	Leu	
	165					170					175					
GTG	GGT	CTC	GTG	GTG	GAG	GGG	GGC	CCT	AAC	GTG	GTG	TCC	ATC	GTC	TTG	930
Val	Gly	Leu	Val	Val	Glu	Gly	Gly	Pro	Asn	Val	Val	Ser	Ile	Val	Leu	
	180				185					190					195	
GAA	TAC	CTG	CAA	GAA	GAG	CCT	CCC	ATC	CCT	GTG	GTG	ATT	TGT	GAT	GGC	978
Glu	Tyr	Leu	Gln	Glu	Glu	Pro	Pro	Ile	Pro	Val	Val	Ile	Cys	Asp	Gly	
				200					205					210		
AGC	GGA	CGT	GCC	TCG	GAC	ATC	CTG	TCC	TTT	GCG	CAC	AAG	TAC	TGT	GAA	1026
Ser	Gly	Arg	Ala	Ser	Asp	Ile	Leu	Ser	Phe	Ala	His	Lys	Tyr	Cys	Glu	
			215					220					225			
GAA	GGC	GGA	ATA	ATA	AAT	GAG	TCC	CTC	AGG	GAG	CAG	CTT	CTA	GTT	ACC	1074
Glu	Gly	Gly	Ile	Ile	Asn	Glu	Ser	Leu	Arg	Glu	Gln	Leu	Leu	Val	Thr	
		230					235					240				
ATT	CAG	AAA	ACA	TTT	AAT	TAT	AAT	AAG	GCA	CAA	TCA	CAT	CAG	CTG	TTT	1122
Ile	Gln	Lys	Thr	Phe	Asn	Tyr	Asn	Lys	Ala	Gln	Ser	His	Gln	Leu	Phe	
	245					250					255					
GCA	ATT	ATA	ATG	GAG	TGC	ATG	AAG	AAG	AAA	GAA	CTC	GTC	ACT	GTG	TTC	1170
Ala	Ile	Ile	Met	Glu	Cys	Met	Lys	Lys	Lys	Glu	Leu	Val	Thr	Val	Phe	
	260				265					270					275	
AGA	ATG	GGT	TCT	GAG	GGC	CAG	CAG	GAC	ATC	GAG	ATG	GCA	ATT	TTA	ACT	1218
Arg	Met	Gly	Ser	Glu	Gly	Gln	Gln	Asp	Ile	Glu	Met	Ala	Ile	Leu	Thr	
				280					285					290		
GCC	CTG	CTG	AAA	GGA	ACA	AAC	GTA	TCT	GCT	CCA	GAT	CAG	CTG	AGC	TTG	1266
Ala	Leu	Leu	Lys	Gly	Thr	Asn	Val	Ser	Ala	Pro	Asp	Gln	Leu	Ser	Leu	
			295					300					305			
GCA	CTG	GCT	TGG	AAC	CGC	GTG	GAC	ATA	GCA	CGA	AGC	CAG	ATC	TTT	GTC	1314
Ala	Leu	Ala	Trp	Asn	Arg	Val	Asp	Ile	Ala	Arg	Ser	Gln	Ile	Phe	Val	
		310					315					320				
TTT	GGG	CCC	CAC	TGG	ACG	CCC	CTG	GGA	AGC	CTG	GCA	CCC	CCG	ACG	GAC	1362
Phe	Gly	Pro	His	Trp	Thr	Pro	Leu	Gly	Ser	Leu	Ala	Pro	Pro	Thr	Asp	
	325					330					335					
AGC	AAA	GCC	ACG	GAG	AAG	GAG	AAG	AAG	CCA	CCC	ATG	GCC	ACC	ACC	AAG	1410
Ser	Lys	Ala	Thr	Glu	Lys	Glu	Lys	Lys	Pro	Pro	Met	Ala	Thr	Thr	Lys	
					345					350					355	
GGA	GGA	AGA	GGA	AAA	GGG	AAA	GGC	AAG	AAG	AAA	GGG	AAA	GTG	AAA	GAG	1458
Gly	Gly	Arg	Gly	Lys	Gly	Lys	Gly	Lys	Lys	Lys	Gly	Lys	Val	Lys	Glu	
				360				365					370			
GAA	GTG	GAG	GAA	GAA	ACT	GAC	CCC	CGG	AAG	ATA	GAG	CTG	CTG	AAC	TGG	1506
Glu	Val	Glu	Glu	Glu	Thr	Asp	Pro	Arg	Lys	Ile	Glu	Leu	Leu	Asn	Trp	
			375					380					385			

GTG AAT GCT TTG GAG CAA GCG ATG CTA GAT GCT TTA GTC TTA GAT CGT Val Asn Ala Leu Glu Gln Ala Met Leu Asp Ala Leu Val Leu Asp Arg 390 395 400	1534
GTC GAC TTT GTG AAG CTC CTG ATT GAA AAC GGA GTG AAC ATG CAA CAC Val Asp Phe Val Lys Leu Ile Glu Asn Gly Val Asn Met Gln His 405 410 415	1602
TTT CTG ACC ATT CCG AGG CTG GAG GAG CTT TAT AAC ACA AGA CTG GGT Phe Leu Thr Ile Pro Arg Leu Glu Glu Leu Tyr Asn Thr Arg Leu Gly 420 425 430 435	1650
CCA CCA AAC ACA CTT CAT CTG CTG GTG AGG GAT GTG AAA AAG AGC AAC Pro Pro Asn Thr Leu His Leu Leu Val Arg Asp Val Lys Lys Ser Asn 440 445 450	1698
CTT CCG CCT GAT TAC CAC ATC AGC CTC ATA GAC ATC GGG CTC GTG CTG Leu Pro Pro Asp Tyr His Ile Ser Leu Ile Asp Ile Gly Leu Val Leu 455 460 465	1746
GAG TAC CTC ATG GGA GGA GCC TAC CGC TGC AAC TAC ACT CGG AAA AAC Glu Tyr Leu Met Gly Gly Ala Tyr Arg Cys Asn Tyr Thr Arg Lys Asn 470 475 480	1794
TTT CGG ACC CTT TAC AAC AAC TTG TTT GGA CCA AAG AGG CCT AAA GCT Phe Arg Thr Leu Tyr Asn Asn Leu Phe Gly Pro Lys Arg Pro Lys Ala 485 490 495	1842
CTT AAA CTT CTG GGA ATG GAA GAT GAT GAG CCT CCA GCT AAA GGG AAG Leu Lys Leu Leu Gly Met Glu Asp Asp Glu Pro Pro Ala Lys Gly Lys 500 505 510 515	1890
AAA AAA AAA AAA AAG AAA AAG GAG GAA GAG ATC GAC ATT GAT GTG GAC Lys Lys Lys Lys Lys Lys Lys Glu Glu Glu Ile Asp Ile Asp Val Asp 520 525 530	1938
GAC CCT GCC GTG AGT CGG TTC CAG TAT CCC TTC CAC GAG CTG ATG GTG Asp Pro Ala Val Ser Arg Phe Gln Tyr Pro Phe His Glu Leu Met Val 535 540 545	1986
TGG GCA GTG CTG ATG AAA CGC CAG AAA ATG GCA GTG TTC CTC TGG CAG Trp Ala Val Leu Met Lys Arg Gln Lys Met Ala Val Phe Leu Trp Gln 550 555 560	2034
CGA GGG GAA GAG AGC ATG GCC AAG GCC CTG GTG GCC TGC AAG CTC TAC Arg Gly Glu Glu Ser Met Ala Lys Ala Leu Val Ala Cys Lys Leu Tyr 565 570 575	2082
AAG GCC ATG GCC CAC GAG TCC TCC GAG AGT GAT CTG GTG GAT GAC ATC Lys Ala Met Ala His Glu Ser Ser Glu Ser Asp Leu Val Asp Asp Ile 580 585 590 595	2130
TCC CAG GAC TTG GAT AAC AAT TCC AAA GAC TTC GGC CAG CTT GCT TTG Ser Gln Asp Leu Asp Asn Asn Ser Lys Asp Phe Gly Gln Leu Ala Leu 600 605 610	2178
GAG TTA TTA GAC CAG TCC TAT AAG CAT GAC GAG CAG ATC GCT ATG AAA Glu Leu Leu Asp Gln Ser Tyr Lys His Asp Glu Gln Ile Ala Met Lys	2226

CCC TAC ATG GGC TAT GGC CGG GTG ATC TAC TGT GTG GAT ATC ATC TTC	2946
Pro Tyr Met Gly Tyr Gly Arg Val Ile Tyr Cys Val Asp Ile Ile Phe	
855 860 865	
TGG TAC ATC CGT GTC CTG GAC ATC TTT GGT GTC AAC AAG TAT CTG GGG	2994
Trp Tyr Ile Arg Val Leu Asp Ile Phe Gly Val Asn Lys Tyr Leu Gly	
870 875 880	
CCA TAC GTG ATG ATG ATT GGA AAG ATG ATG ATC GAC ATG CTG TAC TTT	3042
Pro Tyr Val Met Met Ile Gly Lys Met Met Ile Asp Met Leu Tyr Phe	
885 890 895	
GTG GTC ATC ATG CTG GTC GTG CTC ATG AGT TTC GGA GTA GCC CGT CAA	3090
Val Val Ile Met Leu Val Val Leu Met Ser Phe Gly Val Ala Arg Gln	
900 905 910 915	
GCC ATT CTG CAT CCA GAG GAG AAG CCC TCT TGG AAA CTG GCC CGA AAC	3138
Ala Ile Leu His Pro Glu Glu Lys Pro Ser Trp Lys Leu Ala Arg Asn	
920 925 930	
ATC TTC TAC ATG CCC TAC TGG ATG ATC TAT GGA GAG GTG TTT GCA GAC	3186
Ile Phe Tyr Met Pro Tyr Trp Met Ile Tyr Gly Glu Val Phe Ala Asp	
935 940 945	
CAG ATA GAC CTC TAC GCC ATG GAA ATT AAT CCT CCT TGT GGT GAG AAC	3234
Gln Ile Asp Leu Tyr Ala Met Glu Ile Asn Pro Pro Cys Gly Glu Asn	
950 955 960	
CTA TAT GAT GAG GAG GGC AAG CGG CTT CCT CCC TGT ATC CCC GGC GCC	3282
Leu Tyr Asp Glu Glu Gly Lys Arg Leu Pro Pro Cys Ile Pro Gly Ala	
965 970 975	
TGG CTC ACT CCA GCA CTC ATG GCG TGC TAT CTA CTG GTC GCC AAC ATC	3330
Trp Leu Thr Pro Ala Leu Met Ala Cys Tyr Leu Leu Val Ala Asn Ile	
980 985 990 995	
CTG CTG GTG AAC CTG CTG ATT GCT GTG TTC AAC AAT ACT TTC TTT GAA	3378
Leu Leu Val Asn Leu Leu Ile Ala Val Phe Asn Asn Thr Phe Phe Glu	
1000 1005 1010	
GTA AAA TCA ATA TCC AAC CAG GTG TGG AAG TTC CAG CGA TAT CAG CTG	3426
Val Lys Ser Ile Ser Asn Gln Val Trp Lys Phe Gln Arg Tyr Gln Leu	
1015 1020 1025	
ATT ATG ACA TTT CAT GAC AGG CCA GTC CTG CCC CCA CCG ATG ATC ATT	3474
Ile Met Thr Phe His Asp Arg Pro Val Leu Pro Pro Pro Met Ile Ile	
1030 1035 1040	
TTA AGC CAC ATC TAC ATC ATC ATT ATG CGT CTC AGC GGC CGC TGC AGG	3522
Leu Ser His Ile Tyr Ile Ile Ile Met Arg Leu Ser Gly Arg Cys Arg	
1045 1050 1055	
AAA AAG AGA GAA GGG GAC CAA GAG GAA CGG GAT CGT GGA TTG AAG CTC	3570
Lys Lys Arg Glu Gly Asp Gln Glu Glu Arg Asp Arg Gly Leu Lys Leu	
1060 1065 1070 1075	
TTC CTT AGC GAC GAG GAG CTA AAG AGG CTG CAT GAG TTC GAG GAG CAG	3618
Phe Leu Ser Asp Glu Glu Leu Lys Arg Leu His Glu Phe Glu Glu Gln	

GTG ATA CAT GGA CAG GAC AAA TCA GAT GTT CAA AAC ACT CAG CTA ACA Val Ile His Gly Gln Asp Lys Ser Asp Val Gln Asn Thr Gln Leu Thr 1320 1325 1330	4338
GTG GAA ACG ACA AAT ATA GAA GGC ACT ATT TCC TAT CCC CTG GAA GAA Val Glu Thr Thr Asn Ile Glu Gly Thr Ile Ser Tyr Pro Leu Glu Glu 1335 1340 1345	4386
ACC AAA ATT ACA CGC TAT TTC CCC GAT GAA ACG ATC AAT GCT TGT AAA Thr Lys Ile Thr Arg Tyr Phe Pro Asp Glu Thr Ile Asn Ala Cys Lys 1350 1355 1360	4434
ACA ATG AAG TCC AGA AGC TTC GTC TAT TCC CGG GGA AGA AAG CTG GTC Thr Met Lys Ser Arg Ser Phe Val Tyr Ser Arg Gly Arg Lys Leu Val 1365 1370 1375	4482
GGT GGG GTT AAC CAG GAT GTA GAG TAC AGT TCA ATC ACG GAC CAG CAA Gly Gly Val Asn Gln Asp Val Glu Tyr Ser Ser Ile Thr Asp Gln Gln 1380 1385 1390 1395	4530
TTG ACG ACG GAA TGG CAA TGC CAA GTT CAA AAG ATC ACG CGC TCT CAT Leu Thr Thr Glu Trp Gln Cys Gln Val Gln Lys Ile Thr Arg Ser His 1400 1405 1410	4578
AGC ACA GAT ATT CCT TAC ATT GTG TCG GAA GCT GCA GTG CAA GCT GAG Ser Thr Asp Ile Pro Tyr Ile Val Ser Glu Ala Ala Val Gln Ala Glu 1415 1420 1425	4626
CAA AAA GAG CAG TTT GCA GAT ATG CAA GAT GAA CAC CAT GTC GCT GAA Gln Lys Glu Gln Phe Ala Asp Met Gln Asp Glu His His Val Ala Glu 1430 1435 1440	4674
GCA ATT CCT CGA ATC CCT CGC TTG TCC CTA ACC ATT ACT GAC AGA AAT Ala Ile Pro Arg Ile Pro Arg Leu Ser Leu Thr Ile Thr Asp Arg Asn 1445 1450 1455	4722
GGG ATG GAA AAC TTA CTG TCT GTG AAG CCA GAT CAA ACT TTG GGA TTC Gly Met Glu Asn Leu Leu Ser Val Lys Pro Asp Gln Thr Leu Gly Phe 1460 1465 1470 1475	4770
CCA TCT CTC AGG TCA AAA AGT TTA CAT GGA CAT CCT AGG AAT GTG AAA Pro Ser Leu Arg Ser Lys Ser Leu His Gly His Pro Arg Asn Val Lys 1480 1485 1490	4818
TCC ATT CAG GGA AAG TTA GAC AGA TCT GGA CAT GCC AGT AGT GTA AGC Ser Ile Gln Gly Lys Leu Asp Arg Ser Gly His Ala Ser Ser Val Ser 1495 1500 1505	4866
AGC TTA GTA ATT GTG TCT GGA ATG ACA GCA GAA GAA AAA AAG GTT AAG Ser Leu Val Ile Val Ser Gly Met Thr Ala Glu Glu Lys Lys Val Lys 1510 1515 1520	4914
AAA GAG AAA GCT TCC ACA GAA ACT GAA TGC T AGTCTGTTTT GTTCTTTAA Lys Glu Lys Ala Ser Thr Glu Thr Glu Cys 1525 1530	4965
TTTTTTTTTT TAACAGTCAG AAACCCACTA ATGGGTGTCA TCTTGGCCCA TCCTAAACAC	5025

ATMTCCRAATT TCCTAAAAAC ATTTTCCTT

5055

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1533 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Tyr Ile Arg Val Ser Tyr Asp Thr Lys Pro Asp Ser Leu Leu His
1 5 10 15
Leu Met Val Lys Asp Trp Gln Leu Glu Leu Pro Lys Leu Leu Ile Ser
20 25 30
Val His Gly Gly Leu Gln Asn Phe Glu Met Gln Pro Lys Leu Lys Gln
35 40 45
Val Phe Gly Lys Gly Leu Ile Lys Ala Ala Met Thr Thr Gly Ala Trp
50 55 60
Ile Phe Thr Gly Gly Val Ser Thr Gly Val Ile Ser His Val Gly Asp
65 70 75 80
Ala Leu Lys Asp His Ser Ser Lys Ser Arg Gly Arg Val Cys Ala Ile
85 90 95
Gly Ile Ala Pro Trp Gly Ile Val Glu Asn Lys Glu Asp Leu Val Gly
100 105 110
Lys Asp Val Thr Arg Val Tyr Gln Thr Met Ser Asn Pro Leu Ser Lys
115 120 125
Leu Ser Val Leu Asn Asn Ser His Thr His Phe Ile Leu Ala Asp Asn
130 135 140
Gly Thr Leu Gly Lys Tyr Gly Ala Glu Val Lys Leu Arg Arg Leu Leu
145 150 155 160
Glu Lys His Ile Ser Leu Gln Lys Ile Asn Thr Arg Leu Gly Gln Gly
165 170 175
Val Pro Leu Val Gly Leu Val Val Glu Gly Gly Pro Asn Val Val Ser
180 185 190
Ile Val Leu Glu Tyr Leu Gln Glu Glu Pro Pro Ile Pro Val Val Ile
195 200 205
Cys Asp Gly Ser Gly Arg Ala Ser Asp Ile Leu Ser Phe Ala His Lys
210 215 220
Tyr Cys Glu Glu Gly Gly Ile Ile Asn Glu Ser Leu Arg Glu Gln Leu
225 230 235 240

Leu Val Thr Il Gln Lys Thr Phe Asn Tyr Asn Lys Ala Gln Ser His
 245 250 255
 Gln Leu Phe Ala Ile Ile Met Glu Cys Met Lys Lys Lys Glu Leu Val
 260 265 270
 Thr Val Phe Arg Met Gly Ser Glu Gly Gln Gln Asp Ile Glu Met Ala
 275 280 285
 Ile Leu Thr Ala Leu Leu Lys Gly Thr Asn Val Ser Ala Pro Asp Gln
 290 295 300
 Leu Ser Leu Ala Leu Ala Trp Asn Arg Val Asp Ile Ala Arg Ser Gln
 305 310 315 320
 Ile Phe Val Phe Gly Pro His Trp Thr Pro Leu Gly Ser Leu Ala Pro
 325 330 335
 Pro Thr Asp Ser Lys Ala Thr Glu Lys Glu Lys Lys Pro Pro Met Ala
 340 345 350
 Thr Thr Lys Gly Gly Arg Gly Lys Gly Lys Gly Lys Lys Gly Lys
 355 360 365
 Val Lys Glu Glu Val Glu Glu Glu Thr Asp Pro Arg Lys Ile Glu Leu
 370 375 380
 Leu Asn Trp Val Asn Ala Leu Glu Gln Ala Met Leu Asp Ala Leu Val
 385 390 395 400
 Leu Asp Arg Val Asp Phe Val Lys Leu Leu Ile Glu Asn Gly Val Asn
 405 410 415
 Met Gln His Phe Leu Thr Ile Pro Arg Leu Glu Glu Leu Tyr Asn Thr
 420 425 430
 Arg Leu Gly Pro Pro Asn Thr Leu His Leu Leu Val Arg Asp Val Lys
 435 440 445
 Lys Ser Asn Leu Pro Pro Asp Tyr His Ile Ser Leu Ile Asp Ile Gly
 450 455 460
 Leu Val Leu Glu Tyr Leu Met Gly Gly Ala Tyr Arg Cys Asn Tyr Thr
 465 470 475 480
 Arg Lys Asn Phe Arg Thr Leu Tyr Asn Asn Leu Phe Gly Pro Lys Arg
 485 490 495
 Pro Lys Ala Leu Lys Leu Leu Gly Met Glu Asp Asp Glu Pro Pro Ala
 500 505 510
 Lys Gly Lys Lys Lys Lys Lys Lys Lys Lys Glu Glu Glu Ile Asp Ile
 515 520 525
 Asp Val Asp Asp Pro Ala Val Ser Arg Phe Gln Tyr Pro Phe His Glu
 530 535 540

Leu Met Val Trp Ala Val Leu Met Lys Arg Gln Lys Met Ala Val Phe
 545 550 555 560
 Leu Trp Gln Arg Gly Glu Glu Ser Met Ala Lys Ala Leu Val Ala Cys
 565 570 575
 Lys Leu Tyr Lys Ala Met Ala His Glu Ser Ser Glu Ser Asp Leu Val
 580 585 590
 Asp Asp Ile Ser Gln Asp Leu Asp Asn Asn Ser Lys Asp Phe Gly Gln
 595 600 605
 Leu Ala Leu Glu Leu Leu Asp Gln Ser Tyr Lys His Asp Glu Gln Ile
 610 615 620
 Ala Met Lys Leu Leu Thr Tyr Glu Leu Lys Asn Trp Ser Asn Ser Thr
 625 630 635 640
 Cys Leu Lys Leu Ala Val Ala Ala Lys His Arg Asp Phe Ile Ala His
 645 650 655
 Thr Cys Ser Gln Met Leu Leu Thr Asp Met Trp Met Gly Arg Leu Arg
 660 665 670
 Met Arg Lys Asn Pro Gly Leu Lys Val Ile Met Gly Ile Leu Leu Pro
 675 680 685
 Pro Thr Ile Leu Phe Leu Glu Phe Arg Thr Tyr Asp Asp Phe Ser Tyr
 690 695 700
 Gln Thr Ser Lys Glu Asn Glu Asp Gly Lys Glu Lys Glu Glu Glu Asn
 705 710 715 720
 Thr Asp Ala Asn Ala Asp Ala Gly Ser Arg Lys Gly Asp Glu Glu Asn
 725 730 735
 Glu His Lys Lys Gln Arg Ser Ile Pro Ile Gly Thr Lys Ile Cys Glu
 740 745 750
 Phe Tyr Asn Ala Pro Ile Val Lys Phe Trp Phe Tyr Thr Ile Ser Tyr
 755 760 765
 Leu Gly Tyr Leu Leu Leu Phe Asn Tyr Val Ile Leu Val Arg Met Asp
 770 775 780
 Gly Trp Pro Ser Leu Gln Glu Trp Ile Val Ile Ser Tyr Ile Val Ser
 785 790 795 800
 Leu Ala Leu Glu Lys Ile Arg Glu Ile Leu Met Ser Glu Pro Gly Lys
 805 810 815
 Leu Ser Gln Lys Ile Lys Val Trp Leu Gln Glu Tyr Trp Asn Ile Thr
 820 825 830
 Asp Leu Val Ala Ile Ser Thr Phe Met Ile Gly Ala Ile Leu Arg Leu
 835 840 845

Gln Asn Gln Pro Tyr M t Gly Tyr Gly Arg Val Ile Tyr Cys Val Asp
 850 855 860
 Ile Ile Phe Trp Tyr Ile Arg Val Leu Asp Ile Phe Gly Val Asn Lys
 865 870 875 880
 Tyr Leu Gly Pro Tyr Val Met Met Ile Gly Lys Met Met Ile Asp Met
 885 890 895
 Leu Tyr Phe Val Val Ile Met Leu Val Val Leu Met Ser Phe Gly Val
 900 905 910
 Ala Arg Gln Ala Ile Leu His Pro Glu Glu Lys Pro Ser Trp Lys Leu
 915 920 925
 Ala Arg Asn Ile Phe Tyr Met Pro Tyr Trp Met Ile Tyr Gly Glu Val
 930 935 940
 Phe Ala Asp Gln Ile Asp Leu Tyr Ala Met Glu Ile Asn Pro Pro Cys
 945 950 955 960
 Gly Glu Asn Leu Tyr Asp Glu Glu Gly Lys Arg Leu Pro Pro Cys Ile
 965 970 975
 Pro Gly Ala Trp Leu Thr Pro Ala Leu Met Ala Cys Tyr Leu Leu Val
 980 985 990
 Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Val Phe Asn Asn Thr
 995 1000 1005
 Phe Phe Glu Val Lys Ser Ile Ser Asn Gln Val Trp Lys Phe Gln Arg
 1010 1015 1020
 Tyr Gln Leu Ile Met Thr Phe His Asp Arg Pro Val Leu Pro Pro Pro
 1025 1030 1035 1040
 Met Ile Ile Leu Ser His Ile Tyr Ile Ile Ile Met Arg Leu Ser Gly
 1045 1050 1055
 Arg Cys Arg Lys Lys Arg Glu Gly Asp Gln Glu Glu Arg Asp Arg Gly
 1060 1065 1070
 Leu Lys Leu Phe Leu Ser Asp Glu Glu Leu Lys Arg Leu His Glu Phe
 1075 1080 1085
 Glu Glu Gln Cys Val Gln Glu His Phe Arg Glu Lys Glu Asp Glu Gln
 1090 1095 1100
 Gln Ser Ser Ser Asp Glu Arg Ile Arg Val Thr Ser Glu Arg Val Glu
 1105 1110 1115 1120
 Asn Met Ser Met Arg Leu Glu Glu Ile Asn Glu Arg Glu Thr Phe Met
 1125 1130 1135
 Lys Thr Ser Leu Gln Thr Val Asp Leu Arg Leu Ala Gln Leu Glu Glu
 1140 1145 1150

Leu Ser Asn Arg Met Val Asn Ala Leu Glu Asn Leu Ala Gly Ile Asp
 1155 1160 1165
 Arg Ser Asp Leu Ile Gln Ala Arg Ser Arg Ala Ser Ser Glu Cys Glu
 1170 1175 1180
 Ala Thr Tyr Leu Leu Arg Gln Ser Ser Ile Asn Ser Ala Asp Gly Tyr
 1185 1190 1195 1200
 Ser Leu Tyr Arg Tyr His Phe Asn Gly Glu Glu Leu Leu Phe Glu Asp
 1205 1210 1215
 Thr Ser Leu Ser Thr Ser Pro Gly Thr Gly Val Arg Lys Lys Thr Cys
 1220 1225 1230
 Ser Phe Arg Ile Lys Glu Glu Lys Asp Val Lys Thr His Leu Val Pro
 1235 1240 1245
 Glu Cys Gln Asn Ser Leu His Leu Ser Leu Gly Thr Ser Thr Ser Ala
 1250 1255 1260
 Thr Pro Asp Gly Ser His Leu Ala Val Asp Asp Leu Lys Asn Ala Glu
 1265 1270 1275 1280
 Glu Ser Lys Leu Gly Pro Asp Ile Gly Ile Ser Lys Glu Asp Asp Glu
 1285 1290 1295
 Arg Gln Thr Asp Ser Lys Lys Glu Glu Thr Ile Ser Pro Ser Leu Asn
 1300 1305 1310
 Lys Thr Asp Val Ile His Gly Gln Asp Lys Ser Asp Val Gln Asn Thr
 1315 1320 1325
 Gln Leu Thr Val Glu Thr Thr Asn Ile Glu Gly Thr Ile Ser Tyr Pro
 1330 1335 1340
 Leu Glu Glu Thr Lys Ile Thr Arg Tyr Phe Pro Asp Glu Thr Ile Asn
 1345 1350 1355 1360
 Ala Cys Lys Thr Met Lys Ser Arg Ser Phe Val Tyr Ser Arg Gly Arg
 1365 1370 1375
 Lys Leu Val Gly Gly Val Asn Gln Asp Val Glu Tyr Ser Ser Ile Thr
 1380 1385 1390
 Asp Gln Gln Leu Thr Thr Glu Trp Gln Cys Gln Val Gln Lys Ile Thr
 1395 1400 1405
 Arg Ser His Ser Thr Asp Ile Pro Tyr Ile Val Ser Glu Ala Ala Val
 1410 1415 1420
 Gln Ala Glu Gln Lys Glu Gln Phe Ala Asp Met Gln Asp Glu His His
 1425 1430 1435 1440
 Val Ala Glu Ala Ile Pro Arg Ile Pro Arg Leu Ser Leu Thr Ile Thr
 1445 1450 1455

Asp Arg Asn Gly Met Glu Asn Leu Leu Ser Val Lys Pro Asp Gln Thr
1460 1465 1470

Leu Gly Phe Pro Ser Leu Arg Ser Lys Ser Leu His Gly His Pro Arg
1475 1480 1485

Asn Val Lys Ser Ile Gln Gly Lys Leu Asp Arg Ser Gly His Ala Ser
1490 1495 1500

Ser Val Ser Ser Leu Val Ile Val Ser Gly Met Thr Ala Glu Glu Lys
1505 1510 1515 1520

Lys Val Lys Lys Glu Lys Ala Ser Thr Glu Thr Glu Cys
1525 1530

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